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OM protein - protein search, using sw model

Run on: June 25, 2003, 11:48:15 ; Search time 9.3 Seconds

(without alignments)
66.897 Million cell updates/sec

Title: US-09-869-540a-2_COPY_5_19

Sequence: 1 LRCMLGRVYPCMOV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	165	MLCH_HUMAN	P20382 homo sapien
2	90	100.0	165	MLCH_RAT	P14200 ratu
3	90	100.0	166	MLCH_MOUSE	P56942 mus musculi
4	82	91.1	132	MLC1_ONCKE	P19713 oncorhynch
5	82	91.1	132	MLC1_ONCKI	P56943 oncorhynch
6	82	91.1	132	MLC1_ONCKT	P33745 oncorhynch
7	82	91.1	132	MLC1_ONCKS	P17640 oncorhynch
8	82	91.1	132	MLC2_ONCKE	P19714 oncorhynch
9	82	91.1	136	MLC2_ONCKE	P49794 oreochromis
10	72	80.0	78	MLC2_HUMAN	P016048 homo sapien
11	42	46.7	577	VGLE_PPRV1	P08354 pseudorab
12	42	46.7	3206	POLG_PSBV1	P29152 p genome po
13	41.5	46.1	645	ZP93_MOUSE	O61116 mus musculi
14	41	45.6	124	CD59_XABIT	O77341 oryctolagus
15	41	45.6	315	ISTR_SHISO	P16944 shigella so
16	40.5	45.0	426	S6A_HUMAN	P53796 homo sapien
17	40.5	45.0	635	S6A_HUMAN	P48029 homo sapien
18	40.5	45.0	635	S6A_HUMAN	P31661 oryctolagus
19	40.5	45.0	635	S6A_HUMAN	P28570 ratu
20	40	44.4	1705	PTPO_MOUSE	O64612 ratu
21	40	44.4	1711	PTPO_MOUSE	O64612 ratu
22	39.5	43.9	635	S6A_HUMAN	O18875 bos taurus
23	39.5	43.9	768	BARL_RAT	O99282 ratu
24	39.5	43.9	777	BARL_HUMAN	O99728 ratu
25	39	43.3	111	ORIS_YEAST	P32344 saccharomyc
26	39	43.3	170	HPAC_SALPU	O91922 salmone
27	39	43.3	170	HPAC_SALPU	O82795 salmone
28	39	43.3	170	HPAC_SALPU	O82951 salmone
29	39	43.3	4303	PKD1_HUMAN	P05015 homo sapien
30	38.5	42.8	189	INAP_HUMAN	P05015 homo sapien
31	38.5	42.8	765	BARL_MOUSE	O70445 mus musculi
32	38	42.2	450	CPCL_HUMAN	P33260 homo sapien
33	38	42.2	1011	M3K6_HUMAN	O95382 homo sapien

34	38	42.2	2390	1	SPCP_HUMAN	O15020 homo sapien
35	37	41.1	52	1	REIN_BOVIN	O8117 bos taurus
36	37	41.1	126	1	CD59_PAPSP	O28785 papio sp. (
37	37	41.1	128	1	CD59_CERAP	O28216 cercopithec
38	37	41.1	404	1	HISX_ARCFU	O30027 archaeoglob
39	37	41.1	562	1	RFO3_PETRI	O04716 petunia hyb
40	37	41.1	571	1	PAL4_POPRI	O40910 populus kit
41	37	41.1	662	1	LOXL_MOUSE	P39654 mus musculi
42	37	41.1	666	1	ENY_MLYHO	P21436 homulv mur
43	37	41.1	720	1	MK06_RAT	P27704 ratu
44	37	41.1	721	1	RIR1_MYCPN	P78027 mycoplasma
45	37	41.1	745	1	PERR_HUMAN	P05164 homo sapien

ALIGNMENTS

RESULT 1
MLCH_HUMAN STANDARD; PRT; 165 AA.
ID MLCH_HUMAN
AC P20382; Q16044;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pro-MCH precursor [Contains: Neuropeptide-glycine-glutamic acid (NCP)
DE (Neuropeptide G-E); Neuropeptide-glycine-glutamic acid-iso-leucine (NEI)
DE (Neuropeptide E-I); Melanin-concentrating hormone (MCH)].
GN PMCH OR MCH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE-91125371; PubMed-2149166;
RA Presse F., Nahon J.-L., Fischer W.H., Vale W.;
RT "Structure of the human melanin concentrating hormone mRNA.";
RL Mol. Endocrinol. 4:632-637(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Breast cancer;
RX MEDLINE-93316802; PubMed-8326825;
RA Breton C., Schopp M., Nahon J.-L.;
RT "Isolation and characterization of the human melanin-concentrating
hormone gene and a variant gene.";
RL Brain Res. Mol. Brain Res. 18:297-310(1993).
RN [3]
RP PROCESSING.
RX MEDLINE-99156937; PubMed-10037747;
RA Viale A., Ortolano C., Herlevu G., Furuta M., Barbero P., Steiner D.F.,
RT "Cellular localization and role of pro-hormone convertases in the
processing of pro-melanin concentrating hormone in mammals.";
RL J. Biol. Chem. 274:6536-6545(1999).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE-97334402; PubMed-9191099;
RA Viale A., Zhixing Y., Breton C., Peduto F., Coquerel A., Jordan D.,
RT "The melanin-concentrating hormone gene in human: flanking region
analysis, fine chromosome mapping, and tissue-specific expression.";
RL Brain Res. Mol. Brain Res. 46:243-255(1997).
RN [5]
RP FUNCTION: MCH may act as a neurotransmitter or neuromodulator in a
broad array of neuronal functions directed toward the regulation
of goal-directed behavior, such as food intake, and general
arousal. May also have a role in spermatocyte differentiation.
CC - TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LATERAL
HYPOPHYSIUM. ALSO DETECTED IN PALLIDIUM, NEOCORTEX AND
CEREBELLUM. ALSO FOUND IN THYMUS, BROWN ADIPOSE TISSUE, DUODENUM
AND TESTIS (SPERMATOCYTES AND SEROTI CELLS).
CC NO EXPRESSION IN PERIPHERAL BLOOD. IN BRAIN EXCLUSIVELY NATURE MCH
AND NEI PEPTIDES ARE PRESENT. IN PERIPHERAL TISSUES A LARGE

RL Peptide 19:1317-1327(1998).

CC -1- FUNCTION: MCH inhibits acth secretion at the end of the light on

CC period which corresponds to the peak of the circadian rhythm in

CC ACTH. Inhibits also stress induced ACTH release during the light

CC off period of the cycle. Involved as a neurotransmitter or

CC neuromodulator in a broad array of neuronal functions. Stimulates

CC sexual behavior when injected into the ventromedial nucleus, this

CC effect is antagonized by NEI. In the medial preoptic area,

CC stimulates anxiety and sexual behavior. Antagonizes inhibitory

CC effect of melanotropin alpha on exploration behavior.

CC -1- FUNCTION: NEI CAN INFLUENCE DIFFERENTIATION OF NEURONAL PROCESSES

CC IN BRAIN NEURONS. AFFECTS THE CONTENT OF NEUROFILAMENT PROTEIN IN

CC NEURITOGONESIS (IN VITRO). MAY ALSO BE A NEUROMODULATORY FACTOR.

CC IN BEHAVIORAL TESTS, IT STIMULATES EXPLORATION AND ANXIETY WHEN

CC INJECTED INTO THE VENTROMEDIAL NUCLEUS. ALSO STIMULATES GROOMING,

CC LOCOMOTION AND REARING. MAY ANTAGONIZE THE INHIBITORY EFFECT OF

CC MCH ON ACTH RELEASE. REDUCES DOPAMINE AND DOPAC RELEASE IN THE

CC VENTROMEDIAL NUCLEUS.

CC -1- TISSUE SPECIFICITY: MCH IS PRESENT IN ALL REGIONS OF THE BRAIN AND

CC IN NEUROINTERMEDIATE LOBE OF THE PITUITARY GLAND, WITH HIGHEST

CC CONCENTRATIONS IN THE HYPOTHALAMUS. ALSO EXPRESSED TO A MUCH

CC LESSER EXTENT IN STOMACH, LAMINA PROPRIA OF BOTH DUODENUM AND

CC COLON, OVARY, THYMUS, PANCREAS, ADRENAL GLAND AND TESTIS

CC (SPERMATOGENIA, EARLY SPERMATOCYTES AND SERTOLI CELLS). WEAK

CC EXPRESSION IN HEART AND LUNG. THE OTHER PEPTIDES ARE EXPRESSED AT

CC LEAST IN SERTOLI CELLS, NEI BEING ALSO EXPRESSED IN BRAIN, STOMACH

CC AND PROXIMAL DUODENUM, IN BRAIN EXCLUSIVELY MATURE MCH AND NEI

CC PEPTIDES ARE PRESENT. IN PERIPHERAL TISSUES A LARGE PRODUCT

CC ENCOMPASSING THE NEI AND MCH DOMAINS OF THE PRECURSOR, IS FOUND

CC PREDOMINANTLY. AT LOW LEVELS FULLY PROCESSED MCH AND NEI PEPTIDES

CC ARE PRESENT IN GUT. NO EXPRESSION IN PERIPHERAL BLOOD.

CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS STRONGLY INCREASED IN

CC HYPOTHALAMUS BETWEEN POSTNATAL DAYS 12 AND 20, TO REACH HIGH

CC CONSTANT VALUES IN ADULT.

CC -1- INDUCTION: INHIBITED BY NEUROGENIC STRESS OR OSMOTIC STRESS.

CC -1- PTM: PRO-MCH IS PROCESSED DIFFERENTIALLY IN THE BRAIN AND IN

CC PERIPHERAL ORGANS PRODUCING TWO NEUROPEPTIDES: NEI AND MCH. A

CC THIRD PEPTIDE, NGE, MAY ALSO BE PRODUCED. PREFERENTIAL PROCESSING

CC IN NEURONS BY PROHORMONE CONVERTASE 2 (PC2) GENERATES NEI. MCH IS

CC GENERATED IN NEURONS OF THE LATERAL HYPOTHALAMIC AREA BY SEVERAL

CC PROHORMONE CONVERTASES INCLUDING PC1/3, PC2 AND PCS/6.

CC -1- PTM: MCH IS A CYCLIC PEPTIDE.

CC -1- SIMILARITY: BELONGS TO THE MELANIN-CONCENTRATING HORMONE FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

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DR EMBL: M29712: AAA41580.1: -

DR EMBL: M62641: AAA41581.1: -

DR PIR: A36237: A36237.

DR PIR: A37407: A37407.

KW Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal;

KW Amidation.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 165 PRO-MCH.

FT PEPTIDE 110 128 NGE (POTENTIAL).

FT PEPTIDE 131 143 NEI.

FT PEPTIDE 147 165 MELANIN-CONCENTRATING HORMONE.

FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP).

FT DISULFID 153 162 BY SIMILARITY.

SO SEQUENCE 165 AA: 18482 MW: 3859F07693E77A05 CRC64;

Query Match 100.0%; Score 90; DB 1; Length 165;

Best Local Similarity 100.0%; Pred. No. 6,9e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LRCHMGRYRRCMOV 15

|||||

Db 151 LRCHMGRYRRCMOV 165

RESULT 3

MLCH_MOUSE STANDARD; PRT; 166 AA.

ID MCH_MOUSE

AC P56942;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Pro-MCH precursor [Contains: Neuropeptide-glycine-glutamic acid (NGE)

DE (Neuropeptide G-E); Neuropeptide-glutamic acid-isoleucine (NEI)

DE (Neuropeptide E-I); Melanin-concentrating hormone (MCH)].

GN PMCH OR MCH.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murine; Mus.

OX NCBI_Taxid=10090.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/c; TISSUE-Brain;

RA Breton C., Presse F., Hervieu G., Nahon J.-L.;

RT "Structure and regulation of the mouse melanin-concentrating hormone

RT mRNA and gene.";

RL Mol. Cell. Neurosci. 4:271-284(1993).

RN [2]

RP PROCESSING.

RX MEDLINE-99156937; PubMed-10037747;

RA Viale A., Ortolan C., Hervieu G., Furuta M., Barbero P., Steiner D.F.,

RA Seidah N.G., Nahon J.-L.;

RT "Cellular localization and role of prohormone convertases in the

RT processing of pro-melanin concentrating hormone in mammals.";

RL J. Biol. Chem. 274:6536-6545(1999).

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE-96344052; PubMed-8724342;

RA Hervieu G., Segretain D., Nahon J.-L.;

RT "Developmental and stage-dependent expression of melanin-concentrating

RT hormone in mammalian germ cells.";

RL Biol. Reprod. 54:1161-1172(1996).

CC -1- FUNCTION: MCH may act as a neurotransmitter or neuromodulator in a

CC broad array of neuronal functions directed toward the regulation

CC of goal-directed behavior, such as food intake, and general

CC arousal (By similarity).

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HYPOTHALAMUS. ALSO

CC FOUND IN HEART, INTESTINE, SPLEEN AND TESTIS (SPERMATOGENIA, EARLY

CC SPERMATOCYTES AND SERTOLI CELLS). IN BRAIN ONLY MATURE MCH

CC AND NEI PEPTIDES ARE PRESENT. IN PERIPHERAL TISSUES A LARGE

CC PRODUCT, ENCOMPASSING THE NEI AND MCH DOMAINS OF THE PRECURSOR, IS

CC FOUND PREDOMINANTLY.

CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS ENHANCED BETWEEN POSTNATAL DAYS

CC 10 AND 15.

CC -1- PTM: PRO-MCH IS PROCESSED DIFFERENTIALLY IN THE BRAIN AND IN

CC PERIPHERAL ORGANS PRODUCING TWO NEUROPEPTIDES: NEI AND MCH. A

CC THIRD PEPTIDE, NGE, MAY ALSO BE PRODUCED. PREFERENTIAL PROCESSING

CC IN NEURONS BY PROHORMONE CONVERTASE 2 (PC2) GENERATES NEI. MCH IS

CC GENERATED IN NEURONS OF THE LATERAL HYPOTHALAMIC AREA BY SEVERAL

CC PROHORMONE CONVERTASES INCLUDING PC1/3, PC2 AND PCS/6.

CC -1- PTM: MCH IS A CYCLIC PEPTIDE.

CC -1- SIMILARITY: BELONGS TO THE MCH FAMILY.

DR MGI:97629; Pmch.

KW Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal;

KW Amidation.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 166 PRO-MCH.

FT PEPTIDE 110 129 NGE (POTENTIAL).

FT PEPTIDE 132 144 NEI (BY SIMILARITY).

FT PEPTIDE 148 166 MELANIN-CONCENTRATING HORMONE.

FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)

FT DISULFID 154 163 BY SIMILARITY.

SO SEQUENCE 166 AA: 18645 MW: 13D102686660CA0D CRC64;

Query Match 100.0%; Score 90; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 6, 9e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRCHLGRVTRPCMOV 15
 DB 152 LRCHLGRVTRPCMOV 166

RESULT 4

MLC1_ONCKE STANDARD; PRT; 132 AA.
 ID MLC1_ONCKE P19713; P01208;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PRO-MCH 1 precursor [contains: Neuropeptide-glutamic acid-valine (NEV)
 (Neuropeptide E-V); Melanin-concentrating hormone (MCH)].
 GN MCH1.
 OS Oncorhynchus keta (Chum salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 ON NCBI_TaxID=8018;
 RX SEQUENCE FROM N.A.
 RP MEDLINE-9006787; PubMed-2792771;
 RA Takeyama Y., Wada C., Kawachi H., Ono M.;
 RT Structures of two genes coding for melanin-concentrating hormone of
 RT chum salmon *;
 RL Gene 80:65-73(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89138019; PubMed-2465207;
 RA Ono M., Wada C., Okawa I., Kawachi H.;
 RT Structures of two kinds of mRNA encoding the chum salmon melanin-
 RT concentrating hormone *;
 RL Gene 71:433-438(1988).
 RN [3]
 RP SEQUENCE OF 116-132.
 RX MEDLINE-8601069; PubMed-6621686;
 RA Kawachi H., Kawachi I., Tsubokawa M., Kishida M., Baker B.I.;
 RT Characterization of melanin-concentrating hormone in chum salmon
 RT pituitaries *;
 RL Nature 305:321-323(1983).
 CC -1 FUNCTION: PLAYS A ROLE IN SKIN PIGMENTATION BY ANTAGONIZING THE
 CC ACTION OF MELANOTROPIN ALPHA. INDUCES MELANIN CONCENTRATION WITHIN
 CC THE MELANOPHORES. MAY PARTICIPATE IN THE CONTROL OF THE
 CC HYPOTHALAMO-PITUITARY ADRENAL GLAND AXIS BY INHIBITING THE RELEASE
 CC OF ACTH.
 CC -1 TISSUE SPECIFICITY: PITUITARY GLAND. PRODUCED IN NEURONS OF
 CC LATERAL BASAL HYPOTHALAMUS WHICH PROJECT BOTH TO THE BRAIN AND TO
 CC THE NEURAL LOBE OF THE PITUITARY GLAND FROM WHERE MCH IS RELEASED.
 CC -1 SIMILARITY: BELONGS TO THE MELANIN-CONCENTRATING HORMONE FAMILY.
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 CC -----
 CC EMBL; M27872; AAA49418.1;
 DR EMBL; M23573; AAA49420.1;
 DR PIR; J50282; MTQNIK.
 KW Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal;
 KM Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 132 PRO-MCH 1.
 FT PEPTIDE 101 113 NEV (POTENTIAL).
 FT PEPTIDE 116 132 MELANIN-CONCENTRATING HORMONE.
 FT DISULFID 120 129

FT CONFLICT 4 4 Y -> S (IN REF. 2).
 SQ SEQUENCE 132 AA; 14682 MW; CEECF952924D8738 CRC64;

Query Match 91.1%; Score 82; DB 1; Length 132;
 Best Local Similarity 80.0%; Pred. No. 1, 1e-06;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRCHLGRVTRPCMOV 15
 DB 118 MRCMVGRVTRPCMEV 132

RESULT 5

MLC1_ONCKI STANDARD; PRT; 132 AA.
 ID MLC1_ONCKI P56943;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PRO-MCH 1 precursor [contains: Neuropeptide-glutamic acid-valine (NEV)
 (Neuropeptide E-V); Melanin-concentrating hormone (MCH)].
 GN MCH1.
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 ON NCBI_TaxID=8019;
 RX SEQUENCE FROM N.A.
 RP Nahon J.-L., Presse F., Schoepfer R., Vale W.;
 RT Identification of a single melanin-concentrating hormone messenger
 RT ribonucleic acid in coho salmon: structural relatedness with
 RT ribonucleic acid *;
 RL J. Neuroendocrinol. 3:173-183(1991).
 CC -1 FUNCTION: PLAYS A ROLE IN SKIN PIGMENTATION BY ANTAGONIZING THE
 CC ACTION OF MELANOTROPIN ALPHA. INDUCES MELANIN CONCENTRATION WITHIN
 CC THE MELANOPHORES. MAY PARTICIPATE IN THE CONTROL OF THE
 CC HYPOTHALAMO-PITUITARY ADRENAL GLAND AXIS BY INHIBITING THE RELEASE
 CC OF ACTH.
 CC -1 TISSUE SPECIFICITY: PITUITARY GLAND. PRODUCED IN NEURONS OF
 CC LATERAL BASAL HYPOTHALAMUS WHICH PROJECT BOTH TO THE BRAIN AND TO
 CC THE NEURAL LOBE OF THE PITUITARY GLAND FROM WHERE MCH IS RELEASED.
 CC -1 SIMILARITY: BELONGS TO THE MCH FAMILY.
 CC -----
 CC CLEAVAGE ON PAIR OF BASIC RESIDUES; Hormone; Neuropeptide; Signal;
 KW Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 132 POTENTIAL.
 FT PEPTIDE 101 113 PRO-MCH 1.
 FT PEPTIDE 116 132 NEV (POTENTIAL).
 FT DISULFID 120 129 MELANIN-CONCENTRATING HORMONE.
 FT DOMAIN 86 89 POLY-ALA.
 SQ SEQUENCE 132 AA; 14668 MW; 8B9348336EBB1A8 CRC64;

Query Match 91.1%; Score 82; DB 1; Length 132;
 Best Local Similarity 80.0%; Pred. No. 1, 1e-06;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRCHLGRVTRPCMOV 15
 DB 118 MRCMVGRVTRPCMEV 132

RESULT 6

MLC1_ONCMY STANDARD; PRT; 132 AA.
 ID MLC1_ONCMY P33745;
 AC 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PRO-MCH 1 precursor [contains: Neuropeptide-glutamic acid-valine (NEV)
 (Neuropeptide E-V); Melanin-concentrating hormone (MCH)].
 GN MCH1.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95249052; PubMed=7731499;
RA Baker B., Levy A., Hall L., Lightman S.;
RT Cloning and expression of melanin-concentrating hormone genes in the
RT rainbow trout brain";
RL Neuroendocrinology 61:67-76(1995).
CC -1- FUNCTION: PLAYS A ROLE IN SKIN PIGMENTATION BY ANTAGONIZING THE
CC ACTION OF MELANOTROPIN ALPHA. INDUCES MELANIN CONCENTRATION WITHIN
CC THE MELANOPHORES. MAY PARTICIPATE IN THE CONTROL OF THE
CC HYPOTHALAMO-PITUITARY ADRENAL GLAND AXIS BY INHIBITING THE RELEASE
CC OF ACTH.
CC -1- TISSUE SPECIFICITY: PITUITARY GLAND. PRODUCED IN NEURONS OF
CC LATERAL BASAL HYPOTHALAMUS WHICH PROJECT BOTH TO THE BRAIN AND TO
CC THE NEURAL LOBE OF THE PITUITARY GLAND FROM WHERE MCH IS RELEASED.
CC -1- SIMILARITY: BELONGS TO THE MELANIN-CONCENTRATING HORMONE FAMILY.
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CC -----
DR EMBL: X73837; CAA52059.1;
DR PIR: S34653; S34653.
RW Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal;
KM Multigene family.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 132 PRO-MCH 1.
FT PEPTIDE 101 113 NEV (POTENTIAL).
FT PEPTIDE 116 132 MELANIN-CONCENTRATING HORMONE.
FT DISULFID 120 129 BY SIMILARITY.
SQ SEQUENCE 132 AA; 14608 MW; A0FB644E14C6F99 CRC64;

Query Match 91.1%; Score 82; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 1,1e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRCLMGRRVYRPMQVY 15
Db 118 MRCMVGRRVYRPMQEV 132
:|||||
:|||||

RESULT 7
MCH1_ONCTS STANDARD; PRT; 132 AA.
AC P17640;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pro-MCH 1 precursor [Contains: Neuropeptide-glutamic acid-valine (NEV)
DE (Neuropeptide E-V); Melanin-concentrating hormone (MCH)].
GN MCH1.
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CC NCBI_TaxID=74940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89264605; PubMed=2471200;
RA Minch C.A., Qiu H., Akli H., Watson S.J., Dixon J.E.;
RT "Two precursors of melanin-concentrating hormone: DNA sequence
RT analysis and in situ immunohistochemical localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4292-4296(1989).
CC -1- FUNCTION: PLAYS A ROLE IN SKIN PIGMENTATION BY ANTAGONIZING THE
CC ACTION OF MELANOTROPIN ALPHA. INDUCES MELANIN CONCENTRATION WITHIN

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CC THE MELANOPHORES. MAY PARTICIPATE IN THE CONTROL OF THE
CC HYPOTHALAMO-PITUITARY ADRENAL GLAND AXIS BY INHIBITING THE RELEASE
CC OF ACTH.
CC -1- TISSUE SPECIFICITY: PITUITARY GLAND. PRODUCED IN NEURONS OF
CC LATERAL BASAL HYPOTHALAMUS WHICH PROJECT BOTH TO THE BRAIN AND TO
CC THE NEURAL LOBE OF THE PITUITARY GLAND FROM WHERE MCH IS RELEASED.
CC -1- SIMILARITY: BELONGS TO THE MELANIN-CONCENTRATING HORMONE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M2575; AAA49423.1;
DR PIR: B32910; B32910.
RW Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal;
KM Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 132 PRO-MCH 1.
FT PEPTIDE 101 113 NEV (POTENTIAL).
FT PEPTIDE 116 132 MELANIN-CONCENTRATING HORMONE.
FT DISULFID 120 129
SQ SEQUENCE 132 AA; 14657 MW; F2065B83AFAB46E5 CRC64;

Query Match 91.1%; Score 82; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 1,1e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRCLMGRRVYRPMQVY 15
Db 118 MRCMVGRRVYRPMQEV 132
:|||||
:|||||

RESULT 8
MCH2_ONCKE STANDARD; PRT; 132 AA.
AC P19714; P01208;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pro-MCH 2 precursor [Contains: Neuropeptide-glutamic acid-valine (NEV)
DE (Neuropeptide E-V); Melanin-concentrating hormone (MCH)].
GN MCH2.
OS Oncorhynchus keta (Chum salmon),
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon), and
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CC NCBI_TaxID=8018, 74940, 8022;
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES-O keta; TISSUE-BRAIN;
RA MEDLINE=89263809; PubMed=2471156;
RA Naton J.-L., Schoeffer R., Vale W.;
RT "cDNA sequence of salmon melanin-concentrating hormone exhibits
RT similarities with 7SL RNA.";
RL Nucleic Acids Res. 17:3598-3598(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA SPECIES-O keta;
RA MEDLINE=90006787; PubMed=2792771;
RA Takayama Y., Wada C., Kawachi H., Ono M.;
RT "Structures of two genes coding for melanin-concentrating hormone of
RT chum salmon.";
RL Gene 80:65-73(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA SPECIES-O keta;
RA MEDLINE=89138019; PubMed=2465207;

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RA Breton C., Schorpp M., Nahon J.-L.:
 RT "Isolation and characterization of the human melanin-concentrating
 hormone gene and a variant gene.";
 RL Brain Res. Mol. Brain Res. 18:297-310(1993).
 RN [2]
 RP EXPRESSION.
 RX MEDLINE-98398385; PubMed-9729295;
 RA Miller C.L., Burmeister M., Thompson R.C.:
 RT "Antisense expression of the human pro-melanin-concentrating hormone
 genes.";
 RL Brain Res. 803:86-94(1998).
 CC -1- SIMILARITY: BELONGS TO THE MELANIN-CONCENTRATING HORMONE FAMILY.
 CC -1- CAUTION: PMCHL mRNA MAY NOT BE USED AS TEMPLATE FOR TRANSLATION.
 CC ACCORDING TO REF. 2 ONLY ANTISENSE PMCHL TRANSCRIPTS ARE PRESENT
 IN BRAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S64288; AAB27494.1; -
 DR Genew: HGNC:9110; PMCHL.
 DR MIM: 176793; -
 FT NON_TER 1
 FT DOMAIN 23 41 NGE-LIKE.
 FT DOMAIN 56 56 NEI-LIKE.
 FT DOMAIN 60 78 MELANIN-CONCENTRATING HORMONE-LIKE.
 SQ SEQUENCE 78 AA; 8774 MW; 52826x253D241355 CRC64;
 Query Match 80.0%; Score 72; DB 1; Length 78;
 Best Local Similarity 80.0%; Pred. No. 3; 1e-05;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 LRCHLGRVYRCMOV 15
 Db 64 LSCMLGRVYSCMOV 78
 ID VGLG_PRIVRI STANDARD; PRT; 577 AA.
 AC P08354;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein GI precursor.
 OS Pseudorabies virus (strain Rice) (PRV).
 CC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 CC Alphaherpesvirinae; Varicellovirinae;
 CC NCBI_TaxID=10350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86308235; PubMed-3018284;
 RA Petrovskis E.A., Timmins J.G., Post L.E.:
 RT "Use of lambda gtl to isolate genes for two pseudorabies virus
 RT glycoproteins with homology to herpes simplex virus and varicella-
 RT zoster virus glycoproteins.";
 RL J. Virol. 60:183-193(1986).
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN E FAMILY.
 CC -----
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 CC -----
 DR EMBL: M14336; AAC35205.1; -

DR PIR: B29012; VGBEG1.
 DR Interpro: IPR003404; Herpes_glycoprotein.
 DR Pfam: PF02480; Herpes_gE; 1.
 KW Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 577
 FT CARBOHD 87 87 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHD 93 93 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHD 185 185 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHD 258 258 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHD 343 343 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 577 AA; 62325 MW; AD91F9CBB0EDA69 CRC64;
 Query Match 46.7%; Score 42; DB 1; Length 577;
 Best Local Similarity 63.6%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 RCHLGRVYRC 12
 Db 273 RCHLGRVYRC 283
 ID POLG_PSBMV STANDARD; PRT; 3206 AA.
 AC P29152;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Genome polyprotein [Contains: N-terminal protein (P1); Helper
 DE component proteinase (EC 3.4.22.45) (HC-Pro); protein p3; 6 kDa
 DE protein 1 (6k1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 DE (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
 DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 DE inclusion protein B (NI-B) (RNA-directed RNA polymerase) (EC
 DE 2.7.7.48); Coat protein (CP)].
 OS Pea seed-borne mosaic virus (strain DP1).
 CC Viruses: ssRNA positive-strand viruses, no DNA stage; Polyviridae;
 CC Polyvirus.
 CC NCBI_TaxID=31736;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92044431; PubMed-1940858;
 RA Johansen E., Rasmussen O.F., Heide M., Borkhardt B.:
 RT "The complete nucleotide sequence of pea seed-borne mosaic virus
 RT RNA.";
 RL J. Gen. Virol. 72:2625-2632(1991).
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
 CC further restricted by preferences for the amino acids in p6 - p1,
 CC that vary with the species of polyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
 CC Glu(Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polyprotein, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
 CC [RNA(N)].
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
 CC processing of the polyviral polyprotein.
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PTM: THE VIRAL RNA OF POLYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POLYVIRUSES POLYPEPTIDE FAMILY.
 CC -----

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 CC -----
 DR EMBL; D10930; BAA01726.1; -
 DR PIR; J01331; GNVSPP.
 DR MEROPS; C04.010; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR001730; Peptidase_C4.
 DR InterPro: IPR001456; Peptidase_C6.
 DR InterPro: IPR001540; Poly_P1.
 DR InterPro: IPR001592; Poly_P1.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00767; Poly_coat; 1.
 DR Pfam; PF00851; Peptidase_C6; 1.
 DR Pfam; PF00863; Peptidase_C4; 1.
 DR Pfam; PF01577; Poly_P1; 1.
 DR PRINTS; PR00966; N1POTYPTASE.
 DR SMART; SM00467; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 7 N-TERMINAL PROTEIN.
 FT CHAIN 856 7 HELPER COMPONENT PROTEINASE.
 FT CHAIN 857 7 PROTEIN P3.
 FT CHAIN 1267 1266 6 KDA PROTEIN 1.
 FT CHAIN 1267 1902 CTYLOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1303 1953 6 KDA PROTEIN 2.
 FT CHAIN 1956 7 GENOME-LINKED PROTEIN.
 FT CHAIN 2396 2395 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2396 2915 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2916 3206 COAT PROTEIN.
 FT SITE 1267 1267 CLEAVAGE (BY 49 KDA PROTEASE).
 FT SITE 1902 1903 CLEAVAGE (BY 49 KDA PROTEASE).
 FT SITE 1955 1956 CLEAVAGE (BY 49 KDA PROTEASE).
 FT SITE 2295 2396 CLEAVAGE (BY 49 KDA PROTEASE).
 FT SITE 2395 2396 CLEAVAGE (BY 49 KDA PROTEASE).
 FT SITE 2915 2916 COVALENT LINKAGE OF VIRAL RNA (BY
 FT BINDING 2016 SIMILARITY).
 FT NP_BIND 1351 1358 ATP (POTENTIAL).
 FT SEQUENCE 3206 AA; 364271 MW; 42A3D921BE9ACBF CRC64;
 Query Match 46.7%; Score 42; DB 1; Length 3206;
 Best Local Similarity 40.0%; Pred No. 67;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 LRCMLGRVYRPMOV 15
 Db 437 LAQILRYFPCWRI 451
 RESULT 13
 ZFP3_MOUSE STANDARD; PRT; 645 AA.
 ID ZFP3_MOUSE
 AC Q6116;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein 93 (zfp-93).
 GN ZFP93.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Testis;
 RX MEDLINE=96207307; PubMed=8617494;
 RA Shannon M., Ashworth L.K., Mucenski M.L., Lamerdin J.E., Branscomb E.,
 RA Stubbs L.;
 RT "Comparative analysis of a conserved zinc finger gene cluster on human
 RT chromosome 19q and mouse chromosome 7.",
 RL Genomics 33:112-120(1996).
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 KRAB DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U46186; AAB03529.1; -
 DR HSSP; P25490.12NM.
 DR MGD; MG1:107611; ZFP93.
 DR InterPro: IPR001909; KRAB.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam; PF00096; Zf_C2H2; 13.
 DR Pfam; PF01352; KRAB; 1.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR PRODOM; PD000003; Znf_C2H2; 11.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; Znf_C2H2; 13.
 DR PROSITE; PS50805; ZNF_C2H2; 13.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
 DR Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 KW DOMAIN 8 86 KRAB.
 FT FT 285 643 ZINC FINGERS.
 FT ZN_FING 285 307 C2H2-TYPE.
 FT ZN_FING 313 335 C2H2-TYPE.
 FT ZN_FING 341 363 C2H2-TYPE.
 FT ZN_FING 369 391 C2H2-TYPE.
 FT ZN_FING 397 419 C2H2-TYPE.
 FT ZN_FING 425 447 C2H2-TYPE.
 FT ZN_FING 453 475 C2H2-TYPE.
 FT ZN_FING 481 503 C2H2-TYPE.
 FT ZN_FING 509 531 C2H2-TYPE.
 FT ZN_FING 537 559 C2H2-TYPE.
 FT ZN_FING 565 587 C2H2-TYPE.
 FT ZN_FING 593 615 C2H2-TYPE.
 FT ZN_FING 621 643 C2H2-TYPE.
 FT ZN_FING 643 643 C2H2-TYPE.
 FT SEQUENCE 645 AA; 7459CD140F5AF469 CRC64;
 Query Match 46.1%; Score 41.5; DB 1; Length 645;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 8; Conservative 5; Mismatches 0; Indels 3; Gaps 2;
 QY 1 LRCM-LGRVYRPMOV 15
 Db 63 IRCLPLCOL--PCWOM 76
 RESULT 14
 CD59_RABIT STANDARD; PRT; 124 AA.
 ID CD59_RABIT
 AC O77541;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)


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DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACr) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN C59.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-64.
RC TISSUE-lymphocytes, and Erythrocyte.
RX MEDLINE:9821206; PubMed:9553129;
RA Zhao X.-J., Zhou O., Sims P.J.;
RT "Identity of the residues responsible for the species-restricted
RT complement inhibitory function of human CD59."
RL J. Biol. Chem. 273:10665-10671(1998).
CC -1- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPONENTS OF THE ASSEMBLING MAC, THEREBY PREVENTING
CC INCORPORATION OF THE MULTIPLE COPIES OF C9 REQUIRED FOR COMPLETE
CC FORMATION OF THE OSMOTIC PORE.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -1- MISCELLANEOUS: THE MATURE FORM OF THIS CD59 CONTAINS AN ADDITIONAL
CC SERINE RESIDUE BEFORE THE CONSERVED N-TERMINAL LEUCINE RESIDUE
CC FOUND IN ALL OTHER CD59 HOMOLOGS SEQUENCED TO DATE.
CC -1- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
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CC -----
DR EMBL: AF040387; AAC3590.1; -
DR HSSP: P13987; IERG.
DR InterPro: IPR001526; LY6_UPAR.
DR InterPro: IPR003632; LY-6_CD59.
DR Pfam: PF00021; UPAR_LY6; 1.
DR ProDom: PD003128; LY-6_CD59; 1.
DR SMART: SM00134; LY; 1.
DR PROSITE: PS00983; LY6_UPAR; FALSE_NEG.
DR Antigen: Glycoprotein; GPI-anchor; Signal.
KW SIGNAL.
FT 1 24
FT CHAIN 25 101 CD59 GLYCOPROTEIN.
FT PROPEP 102 124 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 25 101 UPAR/LY6.
FT DISULFID 28 51
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 44 64 BY SIMILARITY.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 89 94 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC...) (POTENTIAL).
FT LIPID 101 101 GPI-ANCHOR (BY SIMILARITY).
SQ SEQUENCE 124 AA; 13870 MW; 13870 MW; CEA64C816772CABD CRC64;

Query Match 45.6%; Score 41; DB 1; Length 124;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 RYRRCMQ 14
DB 59 RYRRCQR 66

RESULT 15
ID ISTR_SHISO STANDARD; PRT; 315 AA.
AC P16944;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Transposase for insertion sequence element IS640.
GN ISTR.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID:624;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:88062685; PubMed:2824781;
RA Matsutani S., Ohtsubo H., Maeda Y., Ohtsubo E.;
RT Isolation and characterization of IS elements repeated in the
RT bacterial chromosome.
RL J. Mol. Biol. 196:445-455(1987).
CC -1- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE IS21/IS408/IS1162 FAMILY OF
CC TRANSPOSASES.
CC -----
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CC -----
DR EMBL: X05956; CAA29390.1; -
DR PIR: S03416; S03416.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00665; Rve; 1.
DR Transposable element: DNA-binding; DNA recombination.
SQ SEQUENCE 315 AA; 37544 MW; DB92FEC677D1D42 CRC64;

Query Match 45.6%; Score 41; DB 1; Length 315;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 CMGRVYRPM 13
DB 305 CVLGQLYRCWM 315

Search completed: June 25, 2003, 11:54:39
Job time : 9.3 secs

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